

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 14:19:05 ; Search time 11.78:seconds

(without alignments)
1279.492 Million cell updates/sec

Title: US-08-883-036a-2

Perfect score: 2327

Sequence: 1 MEORGONAPASGARKRHGP.....HLSSGKFMYLEGNADSAMS 440

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	271.5	11.7	471	1	TNRI_BOVIN
2	243	10.4	461	1	TNRI_PIG
3	218	9.4	454	1	TNRI_MOUSE
4	215	9.2	455	1	TNRI_HUMAN
5	209	9.0	435	1	TNRC_HUMAN
6	203.5	8.7	417	1	WSL1_HUMAN
7	197	8.5	335	1	FASA_HUMAN
8	179.5	7.7	327	1	FASA_MOUSE
9	176.5	7.6	323	1	FASA_BOVIN
10	173.5	7.5	461	1	TNRI_RAT
11	172	7.4	461	1	TNRI_HUMAN
12	170.5	7.3	332	1	FASA_PIG
13	169.5	7.3	435	1	TNRC_MOUSE
14	166	7.1	427	1	NGFR_HUMAN
15	163.5	7.0	474	1	TNRI_MOUSE
16	161.5	6.9	416	1	NGFR_CHICK
17	155	6.7	425	1	NGFR_RAT
18	148.5	6.4	324	1	FASA_RAT
19	142	6.1	272	1	OX40_MOUSE
20	141	6.1	349	1	VC22_VARV
21	139.5	6.0	595	1	CD30_HUMAN
22	137	5.9	271	1	OX40_RAT
23	136.5	5.9	277	1	CD40_HUMAN
24	131.5	5.7	577	1	TBRM_MOUSE
25	131	5.6	2813	1	VWF_CANFA
26	129.5	5.6	277	1	OX40_HUMAN
27	128	5.5	326	1	VT2_MXVL
28	126.5	5.4	519	1	ERR1_HUMAN
29	126	5.4	256	1	41BB_MOUSE
30	122	5.2	462	1	ERR1_MOUSE
31	120	5.2	1808	1	TENA_CHICK
32	118.5	5.1	289	1	CD40_MOUSE
33	118.5	5.1	356	1	TBRM_BOVIN

34	116.5	5.0	575	1	TBRM_HUMAN
35	116	5.0	926	1	EPAL_HUMAN
36	113	4.9	325	1	VT2_SEVKA
37	112	4.8	1436	1	WC11_BOVIN
38	111.5	4.8	667	1	TS11_GIRAL
39	110.5	4.7	655	1	HGRA_HUMAN
40	110.5	4.7	1877	1	PCRS_MOUSE
41	110.5	4.7	2482	1	VWF_PIG
42	110	4.7	250	1	CD27_MOUSE
43	110	4.7	1696	1	PCRS_BRACL
44	109	4.7	2201	1	TENA_HUMAN
45	108.5	4.7	1323	1	LT23_CAEL

ALIGNMENTS

RESULT 1

TNRI_BOVIN STANDARD; PRT; 471 AA.

AC 019131;

DT 01-OCT-2000 (Rel. 40, Created)

DT 01-OCT-2000 (Rel. 40, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-RI) (TNF-RI)

DE (P55).

GN TNFRSF1A OR TNFRI.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Arteria;

RA Lee E.-K., Talyor M.J., Kehli M.E.;

RT "Cloning of cDNA encoding bovine tumor necrosis factor-receptor 1

RT (TNF-RI).";

RT Submitted (FEB-1997) to the EMBL/Genbank/DBJ databases.

CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD

CC RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING

CC AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)

CC PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE

CC SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE

CC PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).

CC -1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFRI LEADS TO

CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS

CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY

CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING

CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO

CC TNFRI COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX

CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND

CC NF-KAPPA B SIGNALING (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.

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CC or send an email to license@sib-sib.ch).

CC

DR EMBL: U90937; AAB65143.1; -

DR HSSP: P19438; ITNR.

DR InterPro: IPR000488; -

DR InterPro: IPR001368; -

DR Pfam: PF00020; TNFR_c6; 3.

DR Pfam: PF00531; death; 1.

DR PROSITE: PS00652; TNFR_NGFR_1; 3.

DR PROSITE: PS50050; TNFR_NGFR_2; 2.

DR PROSITE; PS50017; DEATH DOMAIN; 1.
 KM Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis.
 FT SIGNAL 1 21
 FT CHAIN 22 471
 FT DOMAIN 22 210
 FT TRANSMEM 211 233
 FT DOMAIN 234 471
 FT DOMAIN 43 195
 FT REPEAT 83 82
 FT REPEAT 126 125
 FT REPEAT 126 125
 FT REPEAT 167 195
 FT DOMAIN 360 360
 FT DOMAIN 372 457
 FT DISULFID 44 58
 FT DISULFID 59 72
 FT DISULFID 62 81
 FT DISULFID 84 99
 FT DISULFID 102 117
 FT DISULFID 105 125
 FT DISULFID 127 143
 FT DISULFID 146 158
 FT DISULFID 149 166
 FT DISULFID 168 179
 FT DISULFID 182 190
 FT DISULFID 185 194
 FT CARBOHYD 54 54
 FT CARBOHYD 145 145
 FT CARBOHYD 151 151
 SQ SEQUENCE 471 AA; 51367 MW; 5243EF51ADBE91C4 CRC64;

Query Match 11.7%; Score 271.5; DB 1; Length 471;
 Best Local Similarity 25.2%; Pred No. 4,5e-12;
 Matches 121; Conservative 59; Mismatches 198; Indels 103; Gaps 25;

32 PRVPTLVVAVALLL-----VSAESALITOODLAPQRAAPQOKRSSPSEGL-----CP 82
 4 PIVPGLLEPLVLPALLADYVPAVGVLVPHGDLKRESPPQKYNHPONSTICCTKCH 63
 83 PGHHSIED-----GR--DCISCKYGDYSTHMDLFLCLCTRC--DSGEVELSPCTTTN 134
 64 KQTYLYNDPCPGGRDTCRCVAPG--TYTALENHLRCLSCSRCDMPQVEISPCVVDH 122
 135 TVQCGEEGTFRF--EDSPMCRKCRTPGRCVAVKVDCTPMSDIECVHESG----- 184
 123 TVCGCRKNQYREYWGEGTGRCLNCSL--CENGIVNT--PCQERDPTIC--HGMGFPLKGANC 179
 185 -TKHSGEAPAVEETVTSPT-----PASPCSLGIII--GVVAVALVIVAVCKSL 236
 180 ISCHDCKNKECKLCTPTBSTGKDSODPCTVYLLPLVIVGICLASFASV--VLACRYOR 237
 237 WKKVLPYLKIGSGG-----GDPEVNDK-----SORPAEDVINEIYS--- 277
 238 WK-----PKYLSIIICGSLVKESEPELVAPGFNPPTTTCFSTBSSSVSTIPPYISCDR 294
 278 -----ILOPTQV-----PEQEMEQEPAETGVNMLSPG--ESEHLEPAE 316
 295 SMFGAVASPSSETAPRHLKAGPILPGPASTHLCTPGPASTHLCTPGPASTHLCTPQ 354
 317 AERSORRLLVANECDPTETLRQCFDDPADLVPEDSWEPLMKRLGLMNEIKVAKAENA 376
 355 KWEASAPAPDOLADADPA--TLVAVDG---VPSRKVELVRRLGLSHEIERLENG 409
 377 GH--RDTLYMLIKWVNT-----GRDASVHTLDALETIGERL--AKQIETHL 422
 410 RLRLRAQYSMLAAMRRRPRREATLELLGRVLRDMDLGCLLENIEBALGGAARLASEPRL 469
 423 L 423
 470 L 470

RESULT 2
 ID TNRL_PIG STANDARD; PRT; 461 AA.
 AC P50555;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (TNF-R1) (P55)
 DE (P55)
 GN TNFRSF1A OR TNFR1.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 OX NCBI_Taxid=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=96011645; PubMed=7590278;
 RA Suter B., Pauli U.H.;
 RT *Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.
 RL Gene 163:263-266(1995).
 CC -I- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
 CC -I- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND NF-KAPPA B SIGNALING (BY SIMILARITY).
 CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -I- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC -I- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
 CC -----
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 CC -----
 DR EMBL; U19994; AAC48499.1; -
 DR HSSP; P19438; 1TNR.
 DR InterPro; IPR000488; -
 DR InterPro; IPR01368; -
 DR Pfam; PF00020; TNFR_c6; 3.
 DR Pfam; PF00531; death_1.
 DR PROSITE; PS00652; TNFR_NGFR_1; 3.
 DR PROSITE; PS00650; TNFR_NGFR_2; 2.
 DR PROSITE; PS50017; DEATH DOMAIN; 1.
 KM Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis.
 FT SIGNAL 1 21
 FT CHAIN 22 461
 FT DOMAIN 22 210
 FT TRANSMEM 211 233
 FT DOMAIN 234 461
 FT DOMAIN 43 195
 FT REPEAT 83 82
 FT REPEAT 126 125
 FT REPEAT 126 125
 FT REPEAT 167 195
 FT REPEAT 167 195
 FT DOMAIN 340 350
 FT DOMAIN 362 447
 FT DISULFID 44 58
 FT DISULFID 59 72
 FT DISULFID 62 81

FT DISULFID 84 99 BY SIMILARITY.
 FT DISULFID 102 117 BY SIMILARITY.
 FT DISULFID 105 125 BY SIMILARITY.
 FT DISULFID 127 143 BY SIMILARITY.
 FT DISULFID 146 158 BY SIMILARITY.
 FT DISULFID 149 166 BY SIMILARITY.
 FT DISULFID 168 179 BY SIMILARITY.
 FT DISULFID 182 190 BY SIMILARITY.
 FT DISULFID 185 194 BY SIMILARITY.
 FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 461 AA; 50696 MW; CD72361EC60C9D43 CRC64;

Query Match 10.4%; Score 243; DB 1; Length 461;
 Best Local Similarity 24.6%; Pred. No. 4.4e-10;
 Matches 119; Conservative 61; Mismatches 185; Indels 118; Gaps 26;

QY 30 PGPRVKTLYVVAAYLLV---SASALITQODLAPQORAAQOKRSPSE-----GLC 81
 7 PGLLP-----LVRLALVDYVPAGVGHVLPDREKRESLCQKYSHPQNSICTKC 62
 QY 82 PGCHISED-----GRDCISCKYGODYSTHMDLFCULCTRCDS--GEVELSPCTTR 133
 63 HKGTYLHNDCLGPDLDCECDNG--TFPASENHLTQCISCSCRSBMSQVEISPTVD 121
 QY 134 NTYCOCEEGFREDSPEM--CRKCRGCPRGVAVKGDCTPMAD----- 175
 122 DTVCGCRKNQRYKWSWETLEQCINCSL-CPNGTVOL-PCLEKODTICNCHSGFFLDK 179
 QY 176 IECVH-KESGCKSGEPAVEETVTSPTGPASPCSLGIIIGVVAAYVLYAVFYCKS 234
 180 VSCVGNCKMADCKNL--CPATSETRANDPQDTGTYVLPYFELCLAFLEFV--GLACRY 235
 QY 235 LLMKKVLPYLGKICSGG---GDEPERVDS-----SORPAEDNVLINEIV 276
 236 QRWK---PKLYSTICKGSPFVKEPEPLATAPSPGRTTTFSPISPTTSSPVPSFS 292
 QY 277 SLQPTQVP--EDEMVOEPAE-----PTGVNMLSP-----GSEHLLER 314
 293 PISPTFTPDMSNIRKVTSPPKKIAPPQAGPILMPASTVPVPLPKMGSAHSAHS 352
 QY 315 AAEERQORRLVPAWEGDPTETLRQCFDFAFDPEDSMEPRKLGMDNEI-FYAKA 373
 353 APQOLA-----DADPA-TLYAVNDS---VPTTKKEVYRKLGSSEHIERLELO 397
 QY 374 EAAGHRDLYMLIKWVNTG--RDASVH-----TLDALETGGERL--AKOKIED 420
 398 NGRCLEAGVSMLEWRRRTSREARTELLGSLVRMDLLGCELEIEALRGPARLAPAP 457
 QY 421 HLL 423
 458 HLL 460
 DB
 RESULT 3
 TNRI_MOUSE
 ID TNRI_MOUSE STANDARD: PRT: 454 AA.
 AC P25118;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (TNF-R1) (P55).
 DE TNFRSF1A OR TNFR1 OR TNFR-1.
 GN Mus musculus (Mouse).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE-91187885; PubMed-1849278;
 RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,
 RA Wong G.H., Chen E.Y., Goeddel D.V.;
 RT "Cloning and expression of cDNAs for two distinct murine tumor
 RT necrosis factor receptors demonstrate one receptor is species
 RT specific."
 RT Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).
 RN (2)
 RN SEQUENCE FROM N.A.
 RX MEDLINE-91246168; PubMed-1645445;
 RA Goodwin R.G., Anderson D., Jerry R., Davis T., Brannan C.I.,
 RA Copeland N.G., Jenkins N.A., Smith C.A.;
 RT "Molecular cloning and expression of the type 1 and type 2 murine
 RT receptors for tumor necrosis factor."
 RT Mol. Cell. Biol. 11:3020-3026(1991).
 RN (3)
 RN SEQUENCE FROM N.A.
 RX MEDLINE-91285014; PubMed-1647956;
 RA Barrett K., Taylor-Fishwick D.A., Cope A.P., Kissoneghis A.M.,
 RA Gray P.W., Feldmann M., Foxwell B.M.J.;
 RT "Cloning, expression and cross-linking analysis of the murine p55
 RT tumor necrosis factor receptor."
 RT Eur. J. Immunol. 21:1649-1656(1991).
 RN (4)
 RN SEQUENCE FROM N.A.
 RX TISSUE-Spleen;
 RC MEDLINE-92039815; PubMed-1657766;
 RA Rothe J.G., Brockhaus M., Gentz R., Lesslauer W.;
 RT "Molecular cloning and expression of the mouse Tnf receptor type b."
 RT Immunogenetics 34:338-340(1991).
 RN (5)
 RN SEQUENCE FROM N.A.
 RX MEDLINE-94245292; PubMed-8188324;
 RA Bebo B.F., Linthicum D.S.;
 RT "Nucleotide sequence of the TNF type I receptor from a mouse
 RT endothelioma cell line."
 RT Immunogenetics 39:450-451(1994).
 RN (6)
 RN SEQUENCE FROM N.A.
 RX MEDLINE-93156721; PubMed-8381516;
 RA Rothe J., Bluethmann H., Gentz R., Lesslauer W., Stelmetz M.;
 RT "Genomic organization and promoter function of the murine tumor
 RT necrosis factor receptor beta gene."
 RT Mol. Immunol. 30:165-175(1993).
 RL
 CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
 CC AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
 CC PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
 CC SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
 CC PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
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 CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
 CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
 CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
 CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO
 CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
 CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
 CC NF-KAPPA B SIGNALING (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
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 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: M60468; AAA39751.1; -
 CC EMBL: M59377; AAA40464.1; -
 CC EMBL: X59238; CAA41922.1; -

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DR EMBL: X57796; CAA40936.1; -
DR EMBL: L26349; AAA59361.1; -
DR EMBL: M76556; AAA40465.1; -
DR EMBL: M8067; AAA40465.1; JOINED.
DR EMBL: M7655; AAA40465.1; JOINED.
DR PIR: A3634; GOMST1.
DR PIR: S16677; S16677.
DR PIR: S19021; S19021.
DR HSSP: P19438; 1EXT.
DR MGD: MGI:134884; Tnfstfla.
DR InterPro: IPR000488; -.
DR InterPro: IPR001368; -.
DR Pfam: PF00020; TNFR_C6; 4.
DR PROSITE: PS00531; death; 1.
DR PROSITE: PS00652; TNFR_NGFR_1; 3.
DR PROSITE: PS00500; TNFR_NGFR_2; 3.
DR PROSITE: PS50017; DEATH_DOMAIN; 1.
DR Receptor: Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis.
KW SIGNAL.
FT CHAIN 1 21
FT SIGNAL 1 21
FT CHAIN 22 454
FT SIGNAL 22 454
FT TRANSMEM 22 212
FT TRANSMEM 213 235
FT DOMAIN 236 454
FT DOMAIN 43 196
FT REPEAT 43 82
FT REPEAT 83 125
FT REPEAT 126 166
FT REPEAT 167 196
FT REPEAT 197 349
FT DOMAIN 349 394
FT DOMAIN 394 441
FT DISULFID 44 58
FT DISULFID 59 72
FT DISULFID 73 81
FT DISULFID 82 84
FT DISULFID 85 99
FT DISULFID 102 117
FT DISULFID 102 117
FT DISULFID 127 143
FT DISULFID 146 158
FT DISULFID 146 158
FT DISULFID 168 179
FT DISULFID 182 191
FT DISULFID 185 195
FT CARBOHD 54 54
FT CARBOHD 151 151
FT CARBOHD 202 202
FT CONFLICT 394 394
SQ SEQUENCE 454 AA; 50129 MM; 0710C2E8C3C2B6D9 CRC64;

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Query Match 9.4%; Score 218; DB 1; Length 454;
Best Local Similarity 22.2%; Pred. No. 2.5e-08;
Matches 109; Conservative 51; Mismatches 163; Indels 168; Gaps 22;
OY 32 PVPPTLVVVAVALLLVSAESALITQODLAPQRAAPQOKSSPSEGLCPGHHI----- 87
DB 4 PVPFELLVSLVALLALMGHPSGV---TGLVPS--LGDDEKSDS---LCPVLVILGSHSKN 54
OY 88 -----SEDGRD--CISCKYGDYSTHMDLFLCLCTRC--DSGEVE 125
DB 55 NSICCTCKHKGTYLVSDPSGRDITVCRECKG--FTFASQNLRLCGLCKTKRKMSSQVE 113
OY 126 LSPCTTNTNTVQCGEGTFREDSPDM-----CRCKRTG-----CPRG-M 164
DB 114 ISPCGADKDYCGCKENOFYRLSTHFQCYDVCSPCFMGTYVTPCKETQNTVCNCHAGFF 173
OY 165 VKVGDCPTMSDIECVHKSQSTKHSGEAPAVEETVSSPGRASPCLSGIIGVVAVV 224
DB 174 LRESQVCS--HCKKNECKMLCLPPLAVTNPDSGTAV---LPLVLILGLCILS 227
OY 225 LIVAVFCKSLMKKVLPLYLKIGCSGGGDERVDRSSRGAEDNVINEIVSILOPTOV 284
DB 228 FIFISLMCRYPRM-----RP-----EYYSITICRDPV 253

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OY 285 PROEMVQEPAP-----TGVN-----MSPGSE-----HLEPA 315
DB 254 PVKEKAGPLPPAPSPAPSPSTSGFNPLGTFSTPGSSVSSPTSPILGPSNMHPMPV 313
OY 316 EAKRSQRRLLVPAVEGD-----PTFLRCQDFDA-----DL 348
DB 314 SE-----VPTGQADLLYESLCSVPAPTSYQCKWESAIHPQPDNADLILYAVDG 365
OY 349 VPPDSNEPLMKRLGLMDNEI-KVAAEAAGHDTLYTLIKVNTKGDASYHTLLDALE 407
DB 366 VPPARKKEPRFMGISEHIEIERLEMQNGRCLEAGYSMLDEAWRRTPRHE-----DTLE 419
OY 408 TLGERLAKOKI 418
DB 420 VVGLVLSKMNLL 430

RESULT 4
TNRL_HUMAN STANDARD: PRT: 455 AA.
AC P19438;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (TUMOR NECROSIS FACTOR
GN BINDING PROTEIN 1) (TBPI) (P60) (TNF-RI) (TNF-RI) (P55) (CD120A).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP TISSUE=Placenta;
RC MEDLINE=90235285; PubMed=2158863;
RA Schall T.J., Lewis M., Koller K.J., Lee A., Rice G.C., Wong G.H.W.,
RA Getanaga T., Granger G.A., Lenz R., Raab H., Kohn W.J., Goeddel D.V.;
RT "Molecular cloning and expression of a receptor for human tumor
RL necrosis factor.";
RL Cell 61:361-370(1990).
[2]
RN RP-SEQUENCE FROM N.A.
RX MEDLINE=90235284; PubMed=2158862;
RA Loetscher H., Pan Y.-C.E., Lahm H.-W., Gentz R., Brockhaus M.,
RA Tabuchi H., Lesslauer W.;
RT "Molecular cloning and expression of the human 55 kd tumor necrosis
RL factor receptor.";
RL Cell 61:351-359(1990).
[3]
RN RP-SEQUENCE FROM N.A. AND SEQUENCE OF 41-53; 110-124 AND 199-201.
RX MEDLINE=91006021; PubMed=1698610;
RA Nopar Y., Kemper O., Brakebusch C., Engelmann H., Zhang R.,
RA Aderka D., Holtmann H., Wallach D.;
RT "Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA
RT for the type I TNF-R, cloned using amino acid sequence data of its
RT soluble form, encodes both the cell surface and a soluble form of the
RT receptor.";
RL EMBO J. 9:3269-3278(1990).
[4]
RN RP-SEQUENCE FROM N.A.
RX MEDLINE=91090841; PubMed=1702293;
RA Himmler A., Maurer-Foy I., Kroenke M., Scheurich P., Pflizenmaier K.,
RA Lantz M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;
RT "Molecular cloning and expression of human and rat tumor necrosis
RT factor receptor chain (p60) and its soluble derivative, tumor
RT necrosis factor-binding protein.";
RL DNA Cell Biol. 9:705-715(1990).
[5]
RN RP-SEQUENCE FROM N.A.
RX TISSUE=Placenta;
RX MEDLINE=91017509; PubMed=2170974;
RA Gray P.W., Barrett K., Chantley D., Turner M., Feldman M.;
RT "Cloning of human tumor necrosis factor (TNF) receptor cDNA and

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Db 226 SLF1GLMYRYQRMKSKLYSI--VC--GKSTPEKEGELESTTTKPLAPNPSFSP-----T 276
QY 281 PPGVPEQMEVQAPAPPTGVNMLSPGESEHLLPEAEKRSQRRLVPAPEG----- 332
Db 277 PGTPTPLGSPVPSSTFTSSSTYTPGDCPEAP-----RREVAAPYQGADPLIATA 328
QY 333 ---DPTETLRQCFDDPA-----DLVPEDSWEPLMKLGLMDNEI-KV 370
Db 329 LNSDPIPNPLQKWEKSAHKQSLDTPDPAFLVAVENVPLPKKEFYRRRLGSLDHEIDRL 388
QY 371 AKAAAGHRDLYTLMLIKVYNTK-----GRDASVHTLLDALETGERL 413
Db 389 ELONGRCLEBAQYSMLATWRRTTTPREARETLELLGRVLRMDMLGCELDIEAL 441

RESULT 5
TNRG_HUMAN
ID TNRG_HUMAN STANDARD: PRT; 435 AA.
AC P36941;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE LYMPHOTOXIN-BETA RECEPTOR PRECURSOR (TUMOR NECROSIS FACTOR RECEPTOR
DE 2 RELATED PROTEIN) (TUMOR NECROSIS FACTOR C RECEPTOR).
GN LTBR OR TNFR OR TNFRSF3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA MEDLINE=9352381; PubMed=8486360;
RA Baens M., Chaffanet M., Cassiman J.J., den Bergh H., Marynen P.;
RT "Construction and evaluation of a hncDNA library of human 12p
RT transcribed sequences derived from a somatic cell hybrid.";
RT Genomics 16:214-218(1993).
RN [2]
RP FUNCTION.
RX MEDLINE=94225209; PubMed=8171323;
RX Crowe P.D., van Asdale T.L., Walter B.N., Ware C.F., Hession C.,
RX Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;
RT "A lymphotoxin-beta-specific receptor.";
RT Science 264:707-710(1994).
CC -!- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
CC IMMUNE DEVELOPMENT.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: I04270; AAA36757.1; -
CC HSSP: P25942; ICDF.
DR DR
DR MIM: 600979; -
DR InterPro: IPR001368; -
DR Pfam: PF00020; TNFR_C6; 4.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS50050; TNFR_NGFR_2; 3.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 30
FT CHAIN 31 435
FT DOMAIN 31 227 LYMPHOTOXIN-BETA RECEPTOR.
FT TRASMEM 228 248 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 249 435 POTENTIAL.
FT DOMAIN 42 211 CYTOPLASMIC (POTENTIAL).
FT REPEAT 42 81 4 X TNFR-CYS.
FT REPEAT 82 124 TNFR-CYS 1.
FT REPEAT 82 124 TNFR-CYS 2.

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FT REPEAT 125 168 TNFR-CYS 3.
FT REPEAT 169 211 TNFR-CYS 4..
FT DISULFID 43 58 BY SIMILARITY.
FT DISULFID 59 72 BY SIMILARITY.
FT DISULFID 62 80 BY SIMILARITY.
FT DISULFID 83 98 BY SIMILARITY.
FT DISULFID 101 116 BY SIMILARITY.
FT DISULFID 104 124 BY SIMILARITY.
FT DISULFID 126 132 BY SIMILARITY.
FT DISULFID 139 148 BY SIMILARITY.
FT DISULFID 142 167 BY SIMILARITY.
FT DISULFID 170 185 BY SIMILARITY.
FT CARBOHYD 40 40 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 435 AA; 46709 MW; 624626b6022f56f CRC64;

Query Match 9.0%; Score 209; DB 1; Length 435;
Best Local Similarity 24.5%; Pred. No. 1e-07;
Matches 91; Conservative 39; Mismatches 129; Indels 112; Gaps 18;

QY 20 PGPREARGARPGPRVKTLYVVAVALIVSAESALITQODLAPQGRAPQOKRSSPSE- 78
Db 4 PWATSLAPGLAMGP-----LVGLFGLIAA-----SOPQAVPPYASENQTCRDQKEY 50
QY 79 -----GLCPGHHISEDG--RD--CISCKYQDSTHWNLLFCLRCTCD--SG 122
Db 51 YEPQHRICSCRPGTGYVSAKSRINDYCATCA-ENSYNEHWNLYTLQLCPCDPVWG 109
QY 123 EVLSPCTTTRNTVCCCEBTEFREDSPEMKRCRCRGKAVQVDCIPMSDIE----- 177
Db 110 LEBIAPCTSRKTKQCRQCPQMFCAWALE-CTHCEL-----LSDCPPGTEALKEDEV 160
QY 178 -----CVKESGTRKSGEAPAV-----EETVTSPTGPAS-----PCS 210
Db 161 GKNNHCVCCKAGHPONTSPSPARCPHTRCENQGLVEAPGTAGSDTCKNPLEPPE 220
QY 211 LSGIIGVTY---AAVLIIVAVFCKSLWK-----KVLPTKIGICSGGGGDERVD 259
Db 221 MSGTMLMLAVLPLAFELLATVFSC--IMKSHPSLCKRLGSLKRRQGEQPNV--- 274
QY 260 RSSQRGAEADNVNLEIVSLIPTQ-----VPEQMEVQAPAPPTGV 300
Db 275 AGSWEPKKAHPYFPLVQPLPLISGDVSPVSTGLPAPVLEAGVPOQ---OSPDLTRE 330
QY 301 NMLSPGESEHL 311
Db 331 POLPEGEQSOV 341

RESULT 6
WSL_HUMAN
ID WSL_HUMAN STANDARD: PRT; 417 AA.
AC Q93038; Q93036; Q93037; Q92983; P78515; Q99831; Q99722; P78507;
AC Q99830;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE WSL-1 PROTEIN PRECURSOR (APOPTOSIS-MEDIATING RECEPTOR DR3) (APOPTOSIS-
DE (APOPTOSIS INDUCING TRAMP) (DEATH DOMAIN RECEPTOR 3) (WSL PROTEIN)
DE RECEPTOR OF DEATH) (LARD).
GN TNFRSF12 OR WSL1 OR APO3 OR DR3 OR DDR3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND MUTAGENESIS.
RC TISSUE=Lymphoid;
RA MEDLINE=97088617; PubMed=8934525;
RA Kitson J., Raven T., Jiang Y.-P., Goeddel D.V., Giles K.M., Pun K.-T.,
RA Grilham C.J., Brown R., Farrow S.N.;

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Db 167 PG-----FYENG---DGVSCPTSLGSCPERCAAVCGRMQVWVOLLAGIYVLLLG 217
QY 222 AVLLIYAVFVCKSLMKVLYPYLKIGICSGGDDPERVDSRSQPGADNLTIVSILCP 281
Db 218 ATL-----TYTRHCPHPRVLTADAG---WEALTTPPAVTHLSPLSDAHTLLAP 264
QY 282 TQVPEQEMEVQ-----EPAPFVGNMLSPGES-----EHLLEPAEARSORRLVLP 328
Db 265 PSSSEICIVOLVGNWTFVGYETGALCPQVWMDQLPSRLALGPAAP-----TLSPE 319
QY 329 ANEGDPTFLR---QCFDDPADLVPPDSWEPMLRKIGLMDNEIKVAKAPAGHRTLYTM 385
Db 320 SPAGSPAMMIGPGPOLY-DVMDAVPARRWKEFVRLTGLREAEIYAVEIGRFRDOQYEM 378
QY 386 LKRWKTKGRDASVHTLDDALELIG 410
Db 379 LKRW--RQOQPAAGAVVAALERMG 401

RESULT 7
FASA_HUMAN STANDARD; PRT; 335 AA.
ID FASA_HUMAN STANDARD; PRT; 335 AA.
AC P25445;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)
GN (APO-1 ANTIGEN) (CD95 ANTIGEN).
OS TNFRSF6 OR APT1 OR FAS OR FASL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid:9606;
RN [1]
RP MEDLINE FROM N.A.
RX MEDLINE-91309137; PubMed-1713127;
RA Itoh N., Yonehara S., Ishii A., Yonehara M., Mizushima S.I.,
RA Sameshima M., Hase A., Seto Y., Nagata S.;
RT "The polypeptide encoded by the cDNA for human cell surface antigen
RT Fas can mediate apoptosis."
RL Cell 66:233-243(1991).
RN [2]
RP MEDLINE FROM N.A. AND SEQUENCE OF 226-240; 269-291 AND 321-335.
RX MEDLINE-92268122; PubMed-1375228;
RA Oehm A., Behrmann I., Falk W., Pawlita M., Maier G., Klas C.,
RA Li-Weber M., Richards S., Dhein J., Trauth B.C., Poustingl H.,
RA Krammer P.H.;
RT "Purification and molecular cloning of the APO-1 cell surface
RT antigen, a member of the tumor necrosis factor/nerve growth factor
RT receptor superfamily. Sequence identity with the Fas antigen."
RL J. Biol. Chem. 267:10709-10715(1992).
RN [3]
RP STRUCTURE BY NMR OF 218-335.
RX MEDLINE-97122332; PubMed-8967952;
RA Huang B., Eberstadt M., Olefiniczak E.T., Meadows R.P., Feelik S.W.;
RT "NMR structure and mutagenesis of the Fas (APO-1/CD95) death domain."
RL Nature 384:638-641(1996).
CC -I- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE
CC ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED
CC RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING
CC SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC
CC ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF
CC CASPASES (ASPARATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING
CC APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE
CC INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED
CC SUICIDE OF MATURE T-CELLS, OR BOTH.
CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -I- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC -I- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -I- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -I- DATABASE: NAME=PROW; NOTE=CD guide CD95 entry;

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CC CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd95.htm".
CC -----
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CC -----
DR EMBL: M67454; AAA63174.1; -
DR EMBL: X63717; CAA45250.1; -
DR PIR: A40036; A40036.
DR PIR: S24543; S24543.
DR PDB: IDDE; 12-NOV-97.
DR MIM: 134637; -
DR InterPro: IPR000488; -
DR InterPro: IPR001368; -
DR Pfam: PF00020; TNFR_c6; 2.
DR Pfam: PF00531; death; 1.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS50050; TNFR_NGFR_2; 2.
DR PROSITE: PS50017; DEATH_DOMAIN; 1.
KW Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal;
KW 3D-structure.
FT SIGNAL 1 16
FT CHAIN 17 335 POTENTIAL.
FT DOMAIN 17 173 FASL RECEPTOR.
FT TRANSMEM 174 190 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 191 335 POTENTIAL.
FT DOMAIN 191 335 CYTOPLASMIC (POTENTIAL).
FT REPEAT 47 166 3 X TNFR-CYS.
FT REPEAT 47 83 TNFR-CYS 1.
FT REPEAT 84 127 TNFR-CYS 2.
FT REPEAT 128 166 TNFR-CYS 3.
FT DOMAIN 230 314 DEATH DOMAIN.
FT CARBOHYD 118 118 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 335 AA; 37732 MW; 0139942535111410 CRC64;

Query Match 8.5%; Score 197; DB 1; Length 335;
Best Local Similarity 26.6%; Pred. No. 5.3e-07;
Matches 77; Conservative 34; Mismatches 93; Indels 86; Gaps 14;

QY 38 LVLYAVAVL-----VSAEALITOODLAPQOAAPOQRSSPSSEGL-----CPP 83
Db 8 LPVLYAVARLSKSYNAQVTDINSKGL--ELRKVTYVETONLEGLHNDGFCRKP 65
QY 84 GHH-----ISDGRDCISCKYGDVSTHMDLFLCRLCTCDGSG---EVELSPCTT 134
Db 66 GERKARDCTVNDDEPCVCGQCKEYTDKAFHSSKRCRLCDEGHGLEVEIN-CT 124
QY 135 TVCGCEGEGFREDSPENKCRKRTGCPRGMAVVGCTPMSDIECYHKEGCT----- 185
Db 125 TWCRCRPNFECNSTVCEHDCP--TKCEHGIIL--ECTLTLSNKC--KEGSSNLG 179
QY 186 -----KHSGEPAVEETVYSSPTCPA-----SPCSLSGIITIGVTA 221
Db 180 LLLPIPLIYVAKREYQKTRKHKRENGSHSPILNPETAIVAINISVDLSKYI-- 237
QY 222 AVLLIYAVFVCKSLMKVLYPYLKIGICSGGDDPERVDSRSQPGADNLTIVSILCP 271
Db 238 GVM-----TLSQVKGFVRKNGVNEAKIDEIK-----NDNV 267

RESULT 8
FASA_MOUSE STANDARD; PRT; 327 AA.
ID FASA_MOUSE STANDARD; PRT; 327 AA.
AC P25446;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)

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DE (APO-1 ANTIGEN) (CD95).
DN TNFRSF6 OR APT1 OR FAS.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090.
RN [1]
RP SEQUENCE FROM N.A.
RA Watanabe-Fukunaga R., Brannan C.T., Itoh N., Yonehara S.,
RA Copeland N.G., Jenkins N.A., Nagata S.;
RT "The cDNA structure, expression, and chromosomal assignment of the
RL mouse Fas antigen."
RL J. Immunol. 148:1274-1279(1992).
RN [2]
RP SEQUENCE OF 1-96 FROM N.A.
RA MEDLINE=93189576; PubMed=7680478;
RT Adachi M., Watanabe-Fukunaga R., Nagata S.;
RT "Aberrant transcription caused by the insertion of an early
RT transposable element in an intron of the Fas antigen gene of lpr
RT mice."
RL Proc. Natl. Acad. Sci. U.S.A. 90:1756-1760(1993).
RN [3]
RP VARIANT LPR.
RX MEDLINE=92195401; PubMed=1372394;
RX Watanabe-Fukunaga R., Brannan C.T., Copeland N.G., Jenkins N.A.,
RX Nagata S.;
RT "Lymphoproliferation disorder in mice explained by defects in Fas
RT antigen that mediates apoptosis."
RL Nature 356:314-317(1992).
CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE
CC ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED
CC RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING
CC SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC
CC ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF
CC CASPASES (ASPARATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING
CC APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE
CC INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED
CC SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: DETECTED IN VARIOUS TISSUES INCLUDING THYMUS,
CC LIVER, LUNG, HEART, AND ADUL OVARY.
CC -1- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC -1- DISEASE: DEFECTS IN FAS ARE THE CAUSE OF A LYMPHOPROLIFERATION
CC DISORDER (LPR) RESPONSIBLE FOR LYMPHADENOPATHY AND AUTOANTIBODY
CC PRODUCTION.
CC -1- SIMILARITY: CONTAINS A LA-NGR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
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CC EMBL; M83649; AAA37593.1; -
CC EMBL; S56490; AAB25700.1; -
CC EMBL; S56485; AAB25700.1; JOINED.
CC EMBL; S56486; AAB25700.1; JOINED.
CC PIR; A46484; A46484.
CC HSSP; P25445; IDDE.
CC MGD; MGI:95484; Fas.
CC InterPro; IPR000488; -
CC InterPro; IPR001368; -
CC Pfam; PF00020; TNFR_C6; 3.
CC Pfam; PF00531; death; 1.
CC PROSITE; PS00652; TNFR_NGFR_1; 2.
CC PROSITE; PS00652; TNFR_NGFR_2; 2.
CC PROSITE; PS50017; DEATH_DOMAIN; 1.
CC Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal;
FW

```

[illegible]

CC APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE
 CC INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED
 CC GN SURVIVAL OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
 CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
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 CC -----
 CC EMBL: U34794; AAC48346.1; -.
 CC HSSP: P25445; 1DDF.
 CC InterPro: IPR000488; -.
 CC InterPro: IPR001368; -.
 CC Pfam: PF00020; TNFR_C6; 3.
 CC Pfam: PF00531; death_1.
 CC DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 CC DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 CC DR PROSITE: PS50017; DEATH_DOMAIN; 1.
 CC K1 Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal.
 CC FT SIGNAL 1 16 POTENTIAL.
 CC FT CHAIN 17 323 FASL RECEPTOR.
 CC FT DOMAIN 17 170 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 171 188 POTENTIAL.
 CC FT DOMAIN 189 323 CYTOPLASMIC (POTENTIAL).
 CC FT DOMAIN 45 163 3 X TNFR-CYS.
 CC FT REPEAT 45 80 TNFR-CYS 1.
 CC FT REPEAT 81 124 TNFR-CYS 2.
 CC FT REPEAT 125 163 TNFR-CYS 3.
 CC FT DOMAIN 238 306 DEATH DOMAIN.
 CC SO SEQUENCE 323 AA; 36445 MW; 4D8BA90E9E1F4892 CRC64;
 CC
 CC Query Match 7.6%; Score 176.5; DB 1; Length 323;
 CC Best Local Similarity 26.8%; Pred. No. 1.4e-05;
 CC Matches 68; Conservative 35; Mismatches 88; Indels 63; Gaps 14;
 CC
 CC QY 74 SSPSEGL-----CPGHHSIEDGR-----DCISCKYGDYS--THNNDLFLCLR 115
 CC Db 43 NSCGGLVREHFOCCGPPKRRKNGDCKRODTPCYVLCSSGNETYDKSHSDK--CIR 100
 CC QY 116 CTRCDG---EVELSPCTTNTVCCCEBGTFRREDSPEMKCKRTGCPRGWVKGDCIP 172
 CC Db 101 CICEDEHGLEVEON-CTRTNTKCRCKSNFPCNSPCENCPCTT-CEHGITE--KCTP 156
 CC QY 173 WSDICVAKSESTKSGEAPAEETVTSPPGPAISGIIIGVTAAYAVLIYAVFPC 232
 CC Db 157 TSNKYC-----KGRSHANSIMALLI--LLPIVLII-YKVV 190
 CC QY 233 KSLMKVLYPLKIGICSGGG---DPERVDRSSQRP-AEDVNLNVIYSILOPTVPEGE 288
 CC Db 191 KSRBNKNDKNSAASNDGRLNLTVDDLGKILPISIAEQRIEVEVEFKNMEEK 250
 CC QY 289 ME-----VQEPAE 296
 CC Db 251 IDDIMHDVHETAE 264
 CC
 CC RESULT 10
 CC ID TNRI_RAT STANDARD; PRT; 461 AA.
 CC AC P22934;
 CC DT 01-AUG-1991 (Rel. 19, Created)
 CC DT 01-MAR-1992 (Rel. 21, Last sequence update)
 CC DT 01-OCT-2000 (Rel. 40, Last annotation update)
 CC DE TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (TNF-R1)

DE (P55).
 DE TNFRSF1A OR TNFR1 OR TNFR-1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91090841; PubMed=1702293;
 RA Himmeler A., Maurer-Fogy I., Kroenke M., Scheurich P., Pfizenmaier K.,
 RA Lantz M., Olsson I., Hauptmann R., Stratawa C., Adolf G.R.,
 RT "Molecular cloning and expression of human and rat tumor necrosis
 RT factor receptor chain (p60) and its soluble derivative, tumor
 RT necrosis factor-binding protein.";
 RL DNA Cell Biol. 9:705-715(1990).
 CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
 CC RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
 CC AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
 CC PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
 CC SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
 CC PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
 CC -1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
 CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
 CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
 CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
 CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO
 CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
 CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
 CC NF-KAPPA B SIGNALING (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: M63122; AAA42256.1; -.
 CC PIR: B36555; B36555.
 CC HSSP: P19438; 1TNR.
 CC InterPro: IPR000488; -.
 CC InterPro: IPR001368; -.
 CC Pfam: PF00020; TNFR_C6; 4.
 CC Pfam: PF00531; death_1.
 CC DR PROSITE: PS00652; TNFR_NGFR_1; 3.
 CC DR PROSITE: PS50050; TNFR_NGFR_2; 3.
 CC DR PROSITE: PS50017; DEATH_DOMAIN; 1.
 CC K1 Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis.
 CC FT SIGNAL 1 21 POTENTIAL.
 CC FT CHAIN 22 461 TUMOR NECROSIS FACTOR RECEPTOR 1.
 CC FT DOMAIN 22 211 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 212 234 POTENTIAL.
 CC FT DOMAIN 235 461 CYTOPLASMIC (POTENTIAL).
 CC FT DOMAIN 43 196 4 X TNFR-CYS.
 CC FT REPEAT 43 82 TNFR-CYS 1.
 CC FT REPEAT 83 125 TNFR-CYS 2.
 CC FT REPEAT 126 166 TNFR-CYS 3.
 CC FT REPEAT 167 196 TNFR-CYS 4.
 CC FT DOMAIN 344 354 N-SMASE ACTIVATION DOMAIN (NSD).
 CC FT DOMAIN 363 448 DEATH DOMAIN.
 CC FT DISULFD 44 58 BY SIMILARITY.
 CC FT DISULFD 59 72 BY SIMILARITY.
 CC FT DISULFD 62 81 BY SIMILARITY.
 CC FT DISULFD 84 99 BY SIMILARITY.
 CC FT DISULFD 102 117 BY SIMILARITY.
 CC FT DISULFD 105 125 BY SIMILARITY.
 CC FT DISULFD 127 143 BY SIMILARITY.
 CC FT DISULFD 146 158 BY SIMILARITY.
 CC FT DISULFD 149 166 BY SIMILARITY.

FT DISULFID 168 179 BY SIMILARITY.
 FT DISULFID 182 191 BY SIMILARITY.
 FT DISULFID 185 195 BY SIMILARITY.
 FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 201 201 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 461 AA: 50969 MW: EB23C05450FBD202 CRC64;

Query Match 7.58; Score 173.5; DB 1: Length 461;
 Best Local Similarity 21.48; Pred. No. 3.5e-05;
 Matches 107; Conservative 53; Mismatches 168; Indels 171; Gaps 25;

QY 32 PRPKTLVVAVALLL--VSAESALI--TQODLAPQRAAPQKRSSPSEG-----LCP 82
 DB 4 PIVPGLLSLVLLALMLGHPSCVGLVPSLGRKRDNLCPGKTAHPNNSICTCKH 63
 QY 83 PGHNSIED---GRD--CISCKYGDYSTMNDLLFCLRCTRC--DSGEVLSPTTTRN 134
 DB 64 KGTIVSDCPSPQGVCEVCDKG-TFTASQNHVROCLSCCKRKEMFQVEISPKADMD 122
 QY 135 TVQOCCEGTRF--EDSPKCRKCRGCPGMYKV-----GDCTP 172
 DB 123 TVGCKKNOFORVLSETHQCVCDC-SPCFNGTVTIPCKEKQNTVCNCHAGFSLGNECTP 181
 QY 173 WSDIECVHKSSTKHSSEA-----PAVEETVSSPCTPASPCLSGIIGTVAAVLI 226
 DB 182 -----CSH-----CKNDECKKLLPRVANTNPQDSOT-----AVLLPLVIFLGLC 223
 QY 227 VAVFVCKSLT----WKVLPYLKIGCSGGGDPERVYRASSRPGADNVLNETVSLQP 281
 DB 224 LLEFICISLCRYPOW-----RP-----RVYSITCR 249
 QY 282 TVPQEDME-----VOEPAETGVNMLSPG-----SHLLPRAEAE 319
 DB 250 DSAPEVEEGEIVTKRPLTPASIPAFSPNPGFNPLGFTTPRPSHPVSSTPSVFGPS 309
 QY 320 SQRR-----RLVAVPANGDP-----TEFLROCFDFA----- 346
 DB 310 NMHNFPVPEVEVPVTCGADPLLYGSLNPVPIPAVKKEVVAOOROLDTADRAMLYAV 369
 QY 347 -DLVPEDSMEPLRKLGMLDNEI-KVAKAEAGHRDTLYTMLIKWNKTR-----DASY 399
 DB 370 VDGPRPRMKEPRRLIGLSHEIERELONGRCLEAHVYMLEAMRRRTFRHEATLDVVG 429
 QY 400 HTLLD-----ALETLGERL 413
 DB 430 RVLCDMMLRGCLENIRETL 448

RESULT 11
 TNR2_HUMAN STANDARD; PRT; 461 AA.
 ID TNR2_HUMAN
 AC P20333;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR
 BINDING PROTEIN 2) (TNFRI) (P80) (TNF-R2) (P75) (CD120B) (ETANEREPT).
 GN TNFRSF1B OR TNFR2 OR TNFR.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID:9606;
 RX MEDLINE-90260639; PubMed-2160731;
 RA Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,
 Dower S.K., Cosman D., Goodwin R.G.,
 RT "A receptor for tumor necrosis factor defines an unusual family of
 cellular and viral proteins.";
 RL Science 248:1019-1023(1990).
 RN [2]

RP SEQUENCE FROM N.A.
 RX MEDLINE-9104591; PubMed-2172983;
 RA Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,
 RA Hale K.K., Squires C.H., Thompson R.C., Vanlice J.L.;
 RT "A second tumor necrosis factor receptor gene product can shed a
 naturally occurring tumor necrosis factor inhibitor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-96299745; PubMed-8661109;
 RA Beltinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J.,
 RA Lepaslier D., Stallard B.J., Goeddel D.V., Desauvage F.J.;
 RA Brodeur G.M.;
 RT "Physical mapping and genomic structure of the human TNFR2 gene.";
 RL Genomics 35:94-100(1996).
 RN [4]
 RP SEQUENCE OF 116-461 FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE-90349572; PubMed-216946;
 RA Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D.,
 RA Ringold G.M.;
 RT "Complementary DNA cloning of a receptor for tumor necrosis factor
 and demonstration of a shed form of the receptor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).
 RN [5]
 RP SEQUENCE OF 27-31.
 RX MEDLINE-90110215; PubMed-2153136;
 RA Engelmann H., Novick D., Wallach D.;
 RT "Two tumor necrosis factor-binding proteins purified from human
 urine. Evidence for immunological cross-reactivity with cell surface
 tumor necrosis factor receptors.";
 RL J. Biol. Chem. 265:1531-1536(1990).
 RN [6]
 RP SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362.
 RX MEDLINE-91056048; PubMed-2173696;
 RA Loetscher H., Schlaepper E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W.,
 RA Brockhaus M.;
 RT "Purification and partial amino acid sequence analysis of two
 distinct tumor necrosis factor receptors from Hs60 cells.";
 RL J. Biol. Chem. 265:20131-20138(1990).
 RN [7]
 RP CHARACTERIZATION.
 RX MEDLINE-93016040; PubMed-1328224;
 RA Pennica D., Lam V.T., Mize N.K., Weber R.F., Fendly B.M.,
 RA Lipari M.T., Goeddel D.V.;
 RT "Biochemical properties of the 75-kDa tumor necrosis factor receptor.
 Characterization of ligand binding, internalization, and receptor
 phosphorylation.";
 RL J. Biol. Chem. 267:21172-21178(1992).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN TRAF2 COMPLEX.
 RX MEDLINE-99221490; PubMed-10206649;
 RA Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.;
 RT "Structural basis for self-association and receptor recognition of
 human TRAF2.";
 RL Nature 398:533-538(1999).
 CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. HIGH AFFINITY FOR TNA-ALPHA AND
 APPROXIMATELY 5-FOLD LOWER AFFINITY FOR TNF-BETA.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- PTM: PHOSPHORYLATED; MAINLY ON SERINE RESIDUES WITH A VERY LOW
 LEVEL ON THREONINE RESIDUES.
 CC -1- PHARMACEUTICAL: AVAILABLE UNDER THE NAME ENBREL (IMMUNEX AND
 WYETH-AVERST). USED TO TREAT MODERATE TO SEVERE RHEUMATOID
 ARTHRITIS (RA). ENBREL CONSIST OF THE EXTRACELLULAR LIGAND-BINDING
 PORTION OF TNFR2 LINKED TO AN IMMIGLOBULIN FC CHAIN. IT BINDS TO
 CC TNF-ALPHA AND BLOCKS ITS INTERACTIONS WITH RECEPTORS.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC -1- DATABASE: NAME-PROW; NOTE-CD guide CD120b entry;
 CC -1- DATABASE: NAME-Enbrel; NOTE-Clinical information on Enbrel;
 CC WWW="http://www.enbrelinfo.com/";
 CC -----
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DR EMBL: M32315; AAA5929.1; -
 DR EMBL: M35857; AAA63262.1; -
 DR EMBL: U52165; AAC50622.1; -
 DR EMBL: U52157; AAC50622.1; JOINED.
 DR EMBL: U52158; AAC50622.1; JOINED.
 DR EMBL: U52159; AAC50622.1; JOINED.
 DR EMBL: U52160; AAC50622.1; JOINED.
 DR EMBL: U52161; AAC50622.1; JOINED.
 DR EMBL: U52162; AAC50622.1; JOINED.
 DR EMBL: U52163; AAC50622.1; JOINED.
 DR EMBL: U52164; AAC50622.1; JOINED.
 DR EMBL: M55994; AAA56755.1; -
 DR PIR: A35356; A35356.
 DR PIR: A36007; A36007.
 DR PIR: A36475; A36475.
 DR PIR: B35010; B35010.
 DR PIR: A23666; A23666.
 DR PDB: 1CA9; 12-APR-99.
 DR MIM: 191191; -
 DR InterPro: IPR001368; -
 DR Pfam: PF00020; TNFR_C6; 4.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS50050; TNFR_NGFR_2; 4.
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal;
 KW Phosphorylation; Pharmaceutical; 3D-structure.
 FT SIGNAL 1 22
 FT CHAIN 23 461 TUMOR NECROSIS FACTOR RECEPTOR 2.
 FT DOMAIN 23 257 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 258 287 POTENTIAL.
 FT DOMAIN 288 461 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 39 201 4 X TNFR-CYS.
 FT REPEAT 39 76 TNFR-CYS 1.
 FT REPEAT 77 118 TNFR-CYS 2.
 FT REPEAT 119 162 TNFR-CYS 3.
 FT REPEAT 163 201 TNFR-CYS 4.
 FT DISULFID 40 53 BY SIMILARITY.
 FT DISULFID 54 67 BY SIMILARITY.
 FT DISULFID 57 75 BY SIMILARITY.
 FT DISULFID 78 93 BY SIMILARITY.
 FT DISULFID 96 110 BY SIMILARITY.
 FT DISULFID 100 118 BY SIMILARITY.
 FT DISULFID 120 126 BY SIMILARITY.
 FT DISULFID 134 143 BY SIMILARITY.
 FT DISULFID 137 161 BY SIMILARITY.
 FT CARBOHYD 164 179 BY SIMILARITY.
 FT CARBOHYD 171 171 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 193 193 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 141 141 R -> P (IN REF. 4).
 FT CONFLICT 196 196 R -> M (IN REF. 1 AND 3).
 FT CONFLICT 363 363 A -> T (IN REF. 4).
 FT SEQUENCE 461 AA; 48316 MW; 603B580ECD67636F CRC64;

Query Match 7.4%; Score 172; DB 1; Length 461;
 Best Local Similarity 22.4%; Pred. No. 4,4e-05;
 Matches 88; Conservative 40; Mismatches 134; Indels 130; Gaps 17;

OY 81 CPGHH-----ISEDRGRCISCKYGDYSTHNDLFCILRC-TRDCSGVELSPCTTRTN 134
 DB 57 CSPGHAVVECFCKTSDYCDSE-DSTYTGOLMNVWPECLSCGSSDOVETQACTREON 115
 OY 135 TVCQCESTFEEDSPENC-----RCRTGCPKGMVAVGDTCPMSDIECVHKEGSGT--- 185
 DB 116 RICTCRPMYCALSKQEGCRICAPLRKCRPGF--GVARRG--TETSDVVCRCACGTSTN 171
 OY 186 -----KHSGLAP 192

DB 172 TTSSTICRPHOICNVVAIPGNASRDVCTSTSPRSKAPGAVHLPQVYSTRSQHTQPTP 231
 OY 193 ABEVITSS--PGTPASPCSS-----GLIGTVAAVVLIVAVFC--KSLMLKK 239
 DB 232 EPSTASTSTFLPMGPSPAEGSTGDFALPGLIVGT-ALGELLIGVNCYIMQVKK 290
 OY 240 VL-----PYLKIGCSGGGDDPREVDSSQRPAGENVLNEIYSILO--PTQVPEQ 288
 DB 291 PCLQREARVPHLPADKAGTQGEQOHLITAPSSSSSSLESSASALDRAPTRNOQA 350
 OY 289 MEVO-----EPAPETGVNMLSPC-----ESEHLEPAEERSORRLIV 327
 DB 351 PCVEAGAGAEARASTSSSPSGGHGTQVNYVCIVNCCSSDH-----SSQCSSASTM 405
 OY 328 PANEGDPTETLRQCFDDPADLVFPDSWEPLMR 359
 DB 406 GPTDSSPSESPPD-----EQVPFSKECAFR 431

RESULT 12

FASTA_PIG STANDARD; PRT; 332 AA.
 AC 07736;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)
 DE (APO-1 ANTIGEN) (CD95).
 GN Sus scrofa (Pig).
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_Taxid=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.;
 RT *Expression of apoptosis-associated genes in hibernating and stunned
 RT myocardium of pig.*;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE
 CC ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED
 CC RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING
 CC SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC
 CC ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF
 CC CASPASES (ASPARATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING
 CC APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE
 CC INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED
 CC SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
 CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
 CC
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DR EMBL: AJ001202; CAA04596.1; -
 DR InterPro: IPR000488; -
 DR InterPro: IPR001368; -
 DR Pfam: PF00020; TNFR_C6; 3.
 DR Pfam: PF00531; death; 1.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 DR PROSITE: PS50017; DEATH_DOMAIN; 1.
 KW Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal;
 FT SIGNAL 1 16 POTENTIAL.

FT CHAIN 17 332 FAST RECEPTOR.
 FT DOMAIN 17 175 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 176 192 POTENTIAL.
 FT DOMAIN 193 332 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 193 332 3 X TNFR-CYS.
 FT REPEAT 45 164 TNFR-CYS 1.
 FT REPEAT 82 125 TNFR-CYS 2.
 FT REPEAT 126 164 TNFR-CYS 3.
 FT DOMAIN 227 311 DEATH DOMAIN.
 FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 116 116 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 332 AA; 37592 MW; 588B03682756BF1B CRC64;

Query Match 7.3%; Score 170.5; DB 1; Length 332;
 Best Local Similarity 25.4%; Pred. No. 3.9e-05;
 Matches 61; Conservative 34; Mismatches 90; Indels 55; Gaps 10;

OY 81 CPGPHHSED-----GRDCISCKYGDYSTHWNDLFLCRLCTRCDSG---EVELSPCTT 131
 DB 61 CPGKRRHACSTSPGAPQCVPCSEGEDYDKHNSKCRKRCVCGEHGLEVEKN-CTR 119
 OY 132 TRNTVOCCEGEGTREDSPKCKRTGCPRGVAVKGDCTPMSDIECVKESGTHSGEA 191
 DB 120 TQMTKCRCKNFCHTSCCEHCNCTT-CEHGVIE--NCTPTSNKTC----- 163
 OY 192 PAVEETVTSPPGAPSCSLGIIIGTVAAVYLIYAVFCKSLMKKVLPLYKGTCSG 251
 DB 164 -----REVFGASGRSNLHMLALLILPVALYREVKKRCR---RKENGYPKPTISNA 215
 OY 252 GGDPE-ERVDRSS-----ORPGAEDVNLNEIVSLIOTQVPEDEMEV 291
 DB 216 EEPFMKDVGLGKYYIRIARQAMKTEYKDPVRKNGIEETKIDELMD-NPKDIAEQKVL 274

RESULT 13
 TNRC_MOUSE STANDARD; PRT; 415 AA.
 AC P50284;
 ID TNRC_MOUSE
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE LYMPHOTOXIN-BETA RECEPTOR PRECURSOR.
 GN LTR OR TNFR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CVB: TISSUE-Lung;
 RX MEDLINE=96072804; PubMed=7594541;
 RA Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
 RA Browning J.L., Ware C.F.;
 RT "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
 and expression.";
 RT J. Immunol. 155:5280-5288(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96163885; PubMed=8586432;
 RA Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,
 RA Honjo T.;
 RT "The murine lymphotoxin-beta receptor cDNA: Isolation by the signal
 sequence trap and chromosomal mapping.";
 RT Genomics 30:312-319(1995).
 CC -1- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
 CC IMMUNE DEVELOPMENT.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
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 CC or send an email to license@sib-sib.ch).

CC EMBL: U29173; AA68964.1; -
 CC EMBL: L38423; AAB00846.1; -
 CC EMBL: U30798; AA61334.1; -
 CC HSSP: P25942; ICDF.
 DR MGI: 104875; Lbfr.
 DR InterPro: IPR001368; -
 DR Pfam: PF00020; TNFR_C6; 3.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS50050; TNFR_NGFR_2; 3.
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 30
 FT CHAIN 31 415
 FT DOMAIN 31 223
 FT TRANSMEM 224 244
 FT DOMAIN 245 415
 FT DOMAIN 42 213
 FT REPEAT 42 81
 FT REPEAT 82 124
 FT REPEAT 125 170
 FT REPEAT 171 213
 FT DISULFID 43 58
 FT DISULFID 59 72
 FT DISULFID 62 80
 FT DISULFID 83 98
 FT DISULFID 101 116
 FT DISULFID 104 124
 FT DISULFID 126 132
 FT DISULFID 139 150
 FT DISULFID 142 169
 FT DISULFID 172 187
 FT CARBOHYD 40 40
 FT CARBOHYD 179 179
 SQ SEQUENCE 415 AA; 44956 MW; 29B326A566AEF61 CRC64;

Query Match 7.3%; Score 169.5; DB 1; Length 415;
 Best Local Similarity 23.6%; Pred. No. 5.9e-05;
 Matches 76; Conservative 40; Mismatches 125; Indels 81; Gaps 15;

OY 47 LTVASAESALIT-TOODLAPQORAPPOOKRSSPSE-----GLCPGHHI-----SE 89
 DB 17 LLLGLSLVASSQPOLVPPRIENQTCMDQKEYEPMHVCSSRCPRGEFVAVCSRSQ 76
 OY 90 DGRDCISCKYGDYSTHWNDLFLCRLCTRCDSG-EVELSPCTTTRNTVOCCEEG----- 142
 DB 77 D-TVCKTCPR-NSVNEHMLNSTCQLCRPCDIVLGFEEVAPCTSDRAKRCQPGMNCVY 134
 OY 143 -----TFREDSPKCKRTGCPRGVAVKGDCTPMSDIECVKESGTHSGEAP----- 192
 DB 135 LDNECVACEEERVLCO-----PGTEAEVTDIMDVNCVPCPKPGHFNQNTSSPARCQ 188
 OY 193 -----AVEETVTSPPG-----PASPCLSGIIIGTVAAVYLIYAVFCKSL- 235
 DB 189 PHTRCETIGLVEAPAGTISYDTICKNPPRGAMLLAILSLVFLFTTVLACAMRRHP 248
 OY 236 -LWKVLYPYLK-----GICSGGGGDPERVDRS-----SORPGAEDNV--LNE 274
 DB 249 SLCKRKLGTLLKRPGESESPCPAPRADPPIFPLAERLIPMSGDLSPSPAGPTASLEE 308
 OY 275 IVSILQTPQVPEDEMEVQEPAE 296
 DB 309 VVLQOOSPLVQARELEA-EPGE 329

RESULT 14
 NGRF_HUMAN STANDARD; PRT; 427 AA.
 ID NGRF_HUMAN
 AC P08138;

DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
 DE (GP80-LINGFR) (P75 ICD).
 GN NGFR OR TNFRSF16.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87051725; PubMed=3022937;
 RA Johnson D., Iannahan A., Buck C.R., Sehgal A., Morgan C., Mercer E.,
 RA Bothwell M., Chao M.;
 RL "Expression and structure of the human NGF receptor.";
 RL Cell 47:545-554(1986).
 RN [2]
 RP SEQUENCE OF 1-22 FROM N.A.
 RX MEDLINE=89096903; PubMed=2850481;
 RA Sehgal A., Patil N., Chao M.;
 RL "A constitutive promoter directs expression of the nerve growth factor
 receptor gene.";
 RL Mol. Cell. Biol. 8:3160-3167(1988).
 RT -1- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,
 CC NT-3, AND NT-4.
 CC -1- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE
 CC BOND FORMATION.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
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 CC -----
 DR EMBL: M14764; AAB59544.1; -
 DR EMBL: M21621; AAA36363.1; -
 DR PIR: A23218; GQHUN.
 DR HSP: P07174; INGR.
 DR MIM: 162010; -
 DR InterPro: IPR000488; -
 DR InterPro: IPR001368; -
 DR Pfam: PF00020; TNFR_C6; 4.
 DR Pfam: PF00531; death; 1.
 DR PROSITE: PS00652; TNFR_NGFR_1; 3.
 DR PROSITE: PS00650; TNFR_NGFR_2; 4.
 DR PROSITE: PS50017; DEATH_DOMAIN; 1.
 KW Receptor; Neurogenesis; Transmembrane; Glycoprotein; Repeat;
 KW Phosphorylation; Signal.
 FT SIGNAL 1 28
 FT CHAIN 29 427
 FT DOMAIN 29 250
 FT TRANSMEM 251 272
 FT DOMAIN 273 427
 FT DOMAIN 31 189
 FT REPEAT 31 65
 FT REPEAT 66 107
 FT REPEAT 108 147
 FT REPEAT 148 189
 FT DOMAIN 344 421
 FT DISULFID 32 43
 FT DISULFID 44 57
 FT DISULFID 47 64
 FT DISULFID 67 83
 FT DISULFID 86 99
 FT DISULFID 89 107
 FT DISULFID 107

FT DISULFID 109 122 BY SIMILARITY.
 FT DISULFID 125 138 BY SIMILARITY.
 FT DISULFID 128 146 BY SIMILARITY.
 FT DISULFID 149 164 BY SIMILARITY.
 FT DISULFID 167 180 BY SIMILARITY.
 FT DISULFID 170 188 BY SIMILARITY.
 FT DOMAIN 197 248 SER/THR-RICH.
 FT CARBOHYD 60 60 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 427 AA; 45183 MW; B09FA143FB3D625B CRC64.
 Query Match 7.1%; Score 166; DB 1; Length 427;
 Best Local Similarity 20.0%; Pred. No. 0.00011;
 Matches 98; Conservative 54; Mismatches 167; Indels 170; Gaps 20;
 QY 28 ARGPVPRVETLVVVAANVLLVSAESALITQODLAPQORAPQORSSPSBGLCPGHHI 87
 DB 9 AMDGPRILLLLLLGLVS---LGAKAE-----CPTGLY- 37
 OY 88 SEDGRDCISCKYGODY-----STHNDLLE---CLNCTRCDSGEVLS 127
 DB 38 THSGECKKACNLEGVADPCGANOTVCEPCLDVSFTSDVYATPECKPCTECVGLQMSA 97
 OY 128 PCTTRNTVCOCEGTFREDSR--EMCKKRTG-----CPRGMV--- 165
 DB 98 PCVEADDAVCRCAYGYODETTCRCACRCEAGSGLVFCQDKONTVCECPDGTYSDE 157
 OY 166-----KVGDCTPMSDIECVH-----KESGTHSGEA 191
 DB 158 ANHVDPCLEPTVCEPTEROLRECTRMADAECIEIPGRWITSSTPEGSDSTAPSTQEEA 217
 OY 192 PAVEETVTSPP-----TPASPSLSGIITGVVAVVLIVAVFCKSLM 237
 DB 218 PREQDLINASTVAGVYTTWSSQPVYTGTDNLIPVCSILAAVYGLVAFKR--W 275
 OY 238 KVVLPYLKICSGGGDPERDRSSORPGAEEDVNLNIVSLILOPTVPEQEMEVQEPAP 297
 DB 276 NS-----CKQNKQGANSRP-----VNOTPPPEGEKIHSDSGI---SVDSQSLHQQPHQT 322
 OY 298 T--GYNMLSPGSEHLLPFAERERQRRLLVPAENGPTEIQCFFDPFADYLPFSQME 355
 DB 323 TASGQALGGDGLYSSLPAREEVER---LINGSAG-----DTRW 360
 OY 356 PLMRGLGMDNEIKVKAAGAHRDTLYTMLIKWNKGRDASVHTLDALETGERLAK 415
 DB 361 HLAGELGYQPEHIDSFTHACPR---ALLASWA--TQDSATIDALLAL---RRIQR 410
 OY 416 QKIDPHLS 424
 DB 411 ADLVESLCS 419
 RESULT 15
 TNFR2_MOUSE STANDARD; PRT; 474 AA.
 ID TNFR2_MOUSE
 AC P25119; P97893;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TNF-R2) (P75).
 GN TNFRSF1B OR TNFR2 OR TNFR-2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9118785; PubMed=1849278;
 RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,
 RA Wong G.H., Chen E.Y., Goeddel D.V.;
 RT "Cloning and expression of cDNAs for two distinct murine tumor
 RT necrosis factor receptors demonstrate one receptor is species
 RT specific.";

RL Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834 (1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-9146168; PubMed-1645445;
 RA Goodlin R.G., Anderson D., Jerzy R., Davis T., Brannan C.L.;
 RA Copeland N.G., Jenkins N.A., Smith C.A.;
 RT "Molecular cloning and expression of the type 1 and type 2 murine
 RT receptors for tumor necrosis factor.";
 RL Mol. Cell. Biol. 11:3020-3026 (1991).
 RN [3]
 RP SEQUENCE OF 1-26 FROM N.A.
 RA STRAIN-MOD:
 RA Jacob C.O., Liu J.;
 RL Submitted (JAN-1996) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 1-22 FROM N.A.
 RA TISSUE-LIVER;
 RA Kiseoneghis M., Felloes R., Feldmann M., Chernaevsky Y.;
 RL Submitted (MAY-1995) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
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 CC -----
 CC EMBL: M60469; AAA39752.1; -
 DR EMBL: M59378; AAA40463.1; -
 DR EMBL: U39488; AAA85021.1; -
 DR EMBL: X87128; CAA60618.1; -
 DR PIR: B38634; B38634.
 DR HSSP: P19438; INCF.
 DR MGD: MGI:1314883; Tnfstfb.
 DR InterPro: IPR001368; -
 DR pfam: PF00020; TNFR_C6; 4.
 DR PROSITE: PS00662; TNFR_NGFR_1; 2.
 DR PROSITE: PS50050; TNFR_NGFR_2; 3.
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 22
 FT CHAIN 23 474 TUMOR NECROSIS FACTOR RECEPTOR 2.
 FT DOMAIN 23 258 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 259 288 POTENTIAL.
 FT DOMAIN 289 474 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 39 203 4 X TNFR-CYS.
 FT REPEAT 39 77 TNFR-CYS 1.
 FT REPEAT 78 119 TNFR-CYS 2.
 FT REPEAT 120 164 TNFR-CYS 3.
 FT REPEAT 165 203 TNFR-CYS 4.
 FT DISULFID 40 54 BY SIMILARITY.
 FT DISULFID 55 68 BY SIMILARITY.
 FT DISULFID 58 76 BY SIMILARITY.
 FT DISULFID 79 94 BY SIMILARITY.
 FT DISULFID 97 111 BY SIMILARITY.
 FT DISULFID 101 119 BY SIMILARITY.
 FT DISULFID 121 127 BY SIMILARITY.
 FT DISULFID 136 145 BY SIMILARITY.
 FT DISULFID 139 163 BY SIMILARITY.
 FT DISULFID 166 181 BY SIMILARITY.
 FT CARBOHYD 69 69 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 195 195 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 474 AA; 50319 MW; 462EAE398C4D6563 CRC64;

Db 58 CPFGQYVYKHFNCNKTSDTYVACDCEASM-YTQVWVNOFRTCLSCSSCTTDDVEIRACTKQON 116
 QY 135 TVQCEEGTF-----REEDSPENC-----RKCRTG-----CPRGMYVGDCTPW----- 173
 Db 117 RVACAGEGRYCALKTHSGSCRCGRMSKCGPGVASSRAPNGVNLCKACAPGTFSDTTS 176
 QY 174 -----SDIECVHKESGTRK-----SGRAPAVEETVTSSPGT 204
 Db 177 STDVCRPHRICSLALPGNASTDAVCA-PESPTLSAIPRTLYVSOPEPTRSOPLDQEPG 235
 QY 205 PASPCSLT-----GIIGVTAAVVLIVAFVCSLKKVLPYL 244
 Db 236 SQPRLTSLGSTRPIEQSTRKGISLPIGLIVGT-SLGLIMGLVNCILYQK----- 289
 QY 245 KGICSGGGDPREVDSSORPGADENVLNIYSILDP---TQVPEDEMEVQEPAEPTGVN 301
 Db 290 -----KKPSCLQHDQAKVPHVDEKSDQAVGLEQOHLTTTAPSSSSSSLESSASAGDR 341
 QY 302 MLSPGESEHLLPEPAEERSQRR 324
 Db 342 RAPPGCHPQARVMAEAQGEAR 364

Search completed: May 23, 2001, 14:20:35
 Job time: 90 sec

Query Match 7.0%; Score 163.5; DB 1; Length 474;
 Best Local Similarity 21.7%; Pred. No. 0.00018;
 Matches 70; Conservative 31; Mismatches 127; Indels 95; Gaps 13;
 QY 81 CPGGHHISE-----DGRDCISCRYGODYSTHWNDLFLCLNC-TRCDSGEVELSPCTTTRN 134

